

Fig. 1

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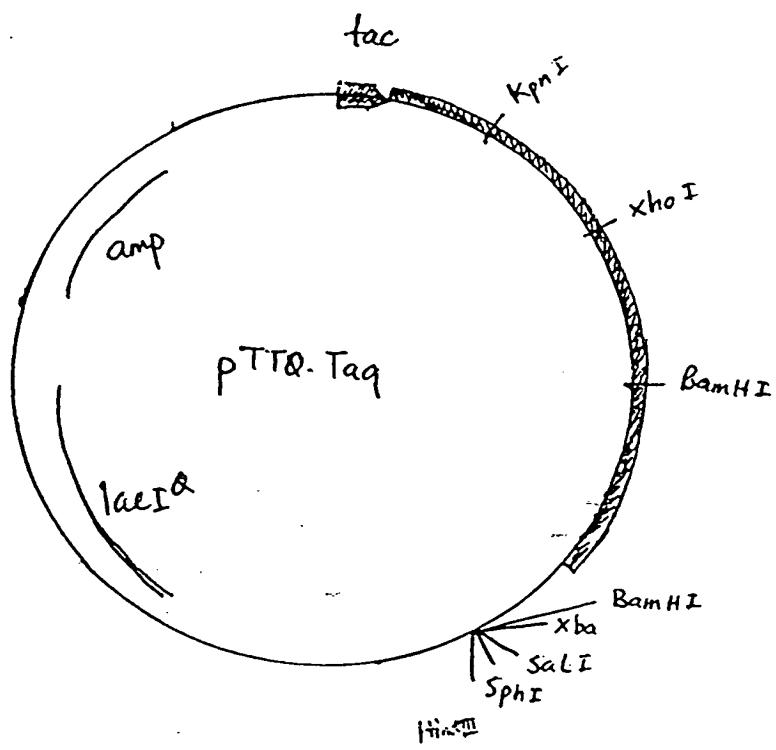
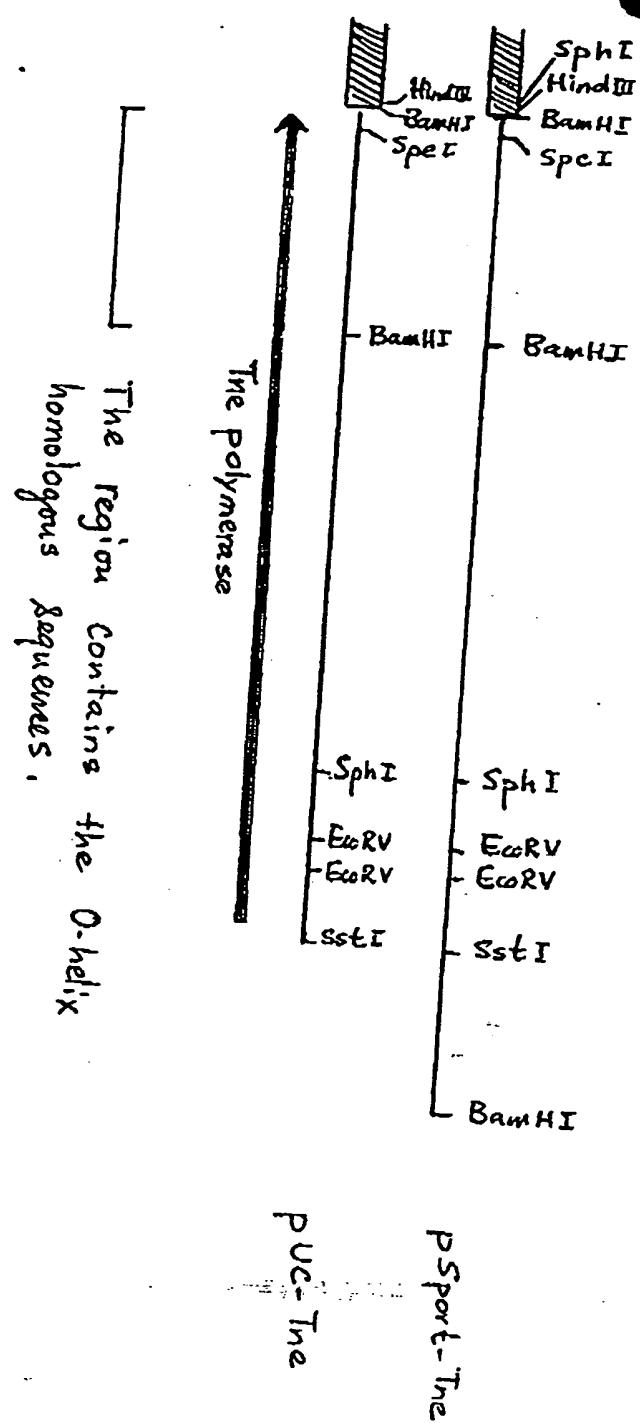


Fig. 2

Fig A



The region contains the O-helix
homologous sequences.

* * * SEQUENCE * * *

BamHI

1 GGATCCAGAC TGGTGGATCG TCAGTGCAGA TTATCCCAA ATAGAACTCA GAATCCTCGC
 → G S R L V D R Q C G L F P N R T Q N P R
 → D P D W W I V S A D Y S Q I E L R I L
 I Q T G G S S V R I I P K - N S E S S

61 TCATCTCAGT GGTGATGAGA ACCTTGTGAA GCCCTTCGAG GAGGGCATCG ATGTGCACAC
 → S S Q W - - E P C E G L R G G H R C A H
 → A H L S G D E N L V K A F E E G I D V H
 L I S V V M R T L - R P S R R A S M C T

121 CTTGACTGCC TCCAGGATCT ACAACGTAAA GCCAGAAGAA GTGAACGAAG AAATGCGACG
 → L D C L Q D L Q R K A R R S E R R N A T
 → T L T A S R I Y N V K P E E V N E E M R
 P - L P P G S T T - S Q K K - T K K C D

181 GGTTGGAAAG ATGGTGAAC TCTCTATAAT ATACGGTGTGTC ACACCGTACG GTCTTCTGT
 → G W K D G E L L Y N I R C H T V R S F C
 → R V G K M V N (F) S I I Y G V T P Y G L S
 G L E R W - T S L - Y T V S H R T V F L

241 GAGACTTGGAA ATACCGGTTA AAGAAGCAGA AAAGATGATT ATCAGCTATT TCACACTGTA
 → E T W N T G - R S R K D D Y Q L F H T V
 → V R L G I P V K E A E K M I I S Y F T L
 → - D L E Y R L K K Q K R - L S A I S H C

301 TCCAAAGGTG CGAAGCTACA TCCAGCAGGT TGGTGCAGAG GCAAAAGAGA AGGGCTACGT
 → S K G A K L H P A G G C R G K R E G L R
 → Y P K V R S Y I Q Q V V A E A K E K G Y
 → I Q R C E A T S S R L L Q R Q K R R A T

361 CAGGACTCTC TTTGGAAGAA AAAGAGATAT TCCCCAGCTC ATGGCAAGGG ACAAGAACAC
 → Q D S L W K K K R Y S P A H G K G Q E H
 → V R T L F G R K R D I P Q L M A R D K N
 → S G L S L E E K E I F P S S W Q G T R T

421 CCAGTCCGAA GGCGAAAGAA TCGCAATAAA CACCCCCATT CAGGAACTG CGGCAGATAT
 → P V R R R K N R N K H P H S G N C G R Y
 → T Q S E G E R I A I N T P I Q G T A A D
 → P S P K A K E S Q - T P P F R E L R Q I

481 AATAAAATTG GCTATGATAG ATATAGACGA GGAGCTGAGA AAAAGAAACA TCAAATCCAG
 → N K I G Y D R Y R R G A E K K K H E I Q
 → I I K L A M I D I D E E L R K R N M K S
 → - N W L - - I - T R S - E K E T - N P

541 AATGATGATT CAGGTTCATG ACCAACTGGT CTTCGAGGT CCCGATGAGG AAAAGAAAGA
 → N D H S G S - R T G L R G S R - G K R R
 → R M I I Q V H D E L V F E V P D E E K E
 → E - S F R F M T N W S S R F P M R K K K

601 ACTAGITGAT CTGGTGAAGA ACAAAATGAC AAATGTGGTG AAAACTCTCTG TGCCTCTTGA
 → T S - S G E E Q N D K C G E T L C A S -
 → E L V D L V K N K M T N V V K L S V P L
 → N - L I W - R T K - Q M W - N S L C L L

Fig 4

661 GGTTGACATA AGCATCGGAA A [REDACTED] GTC TTGA
G - H K H R K [REDACTED] L V L
→ E V D I S I G K S W S -
R L T - A S E K A G L

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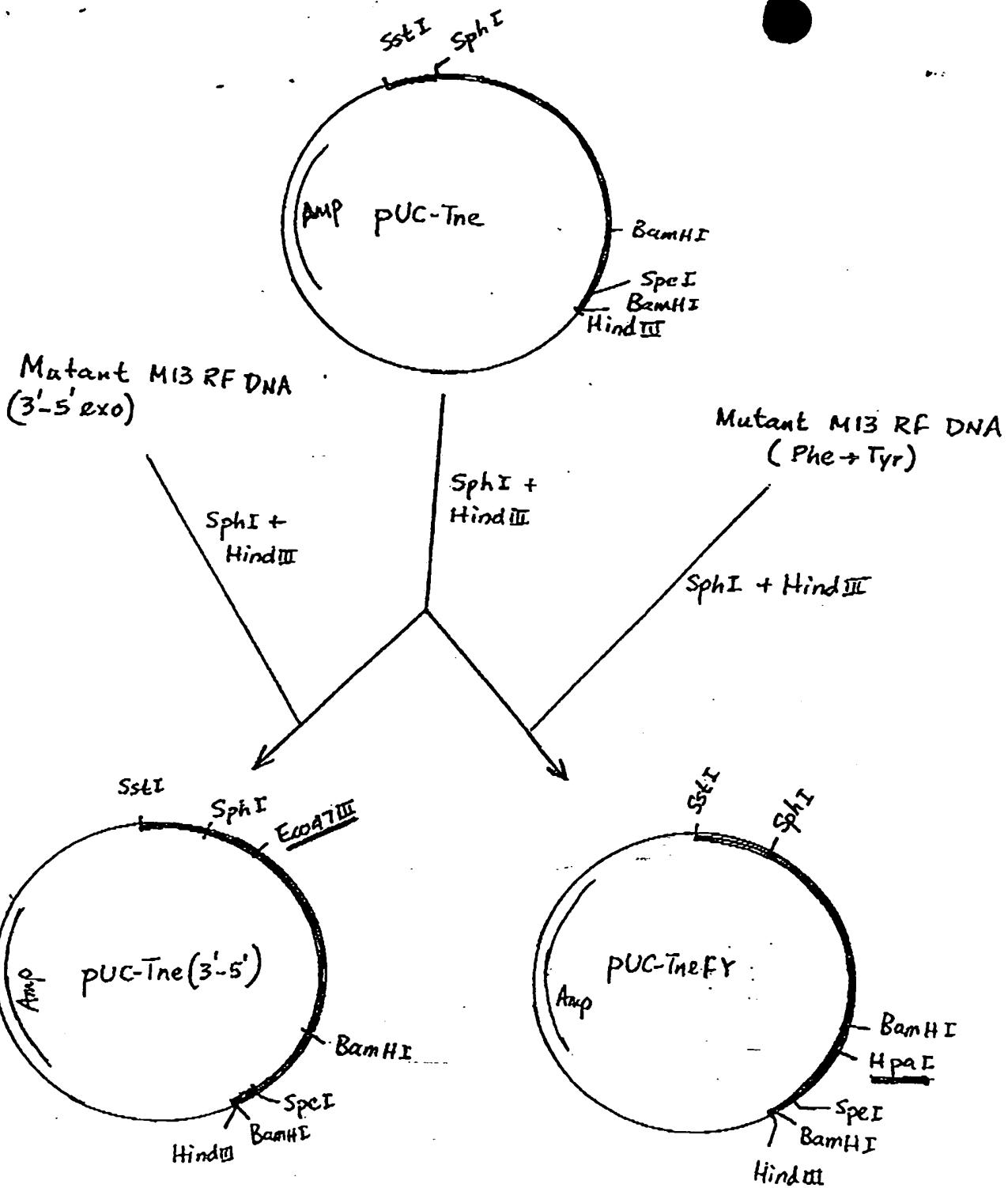
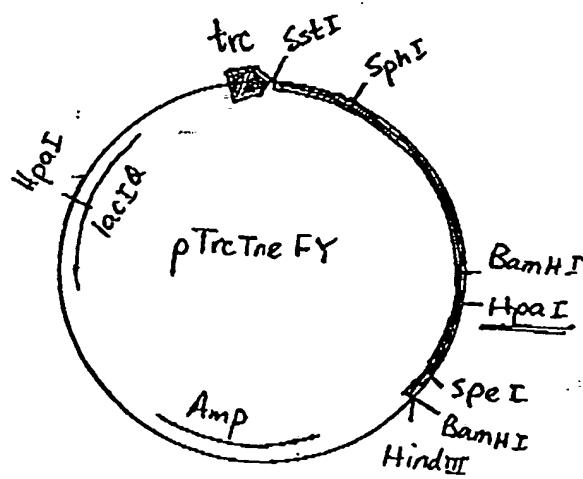
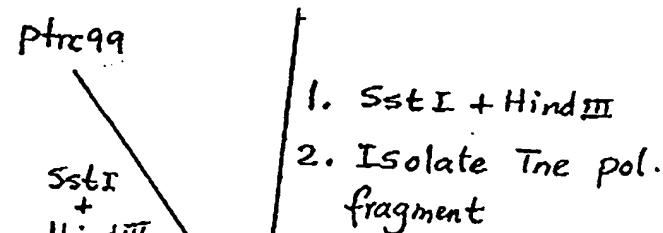
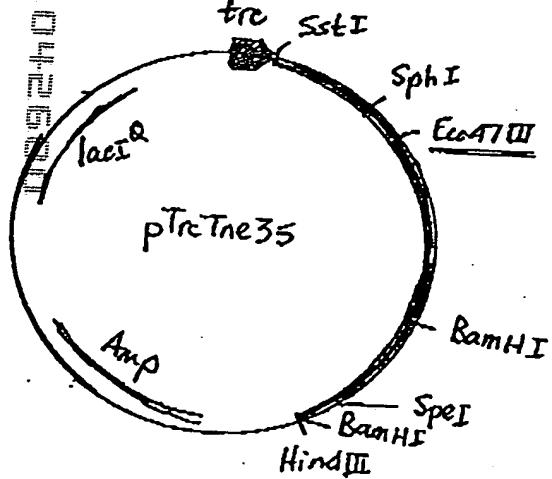
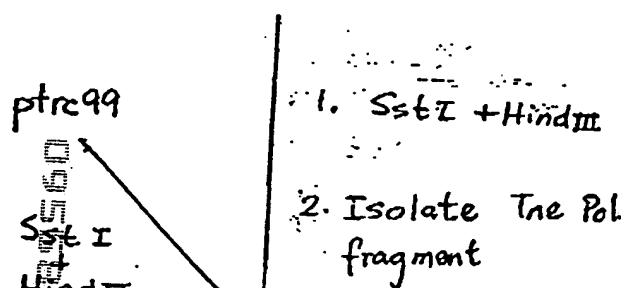
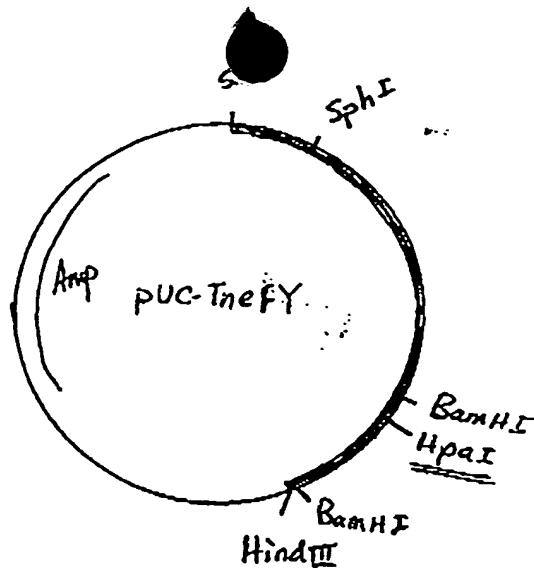
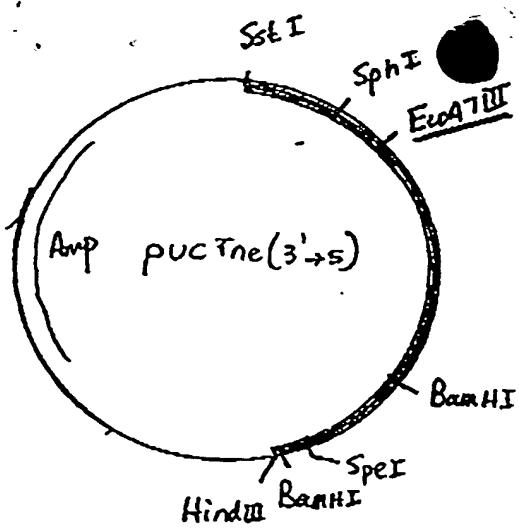
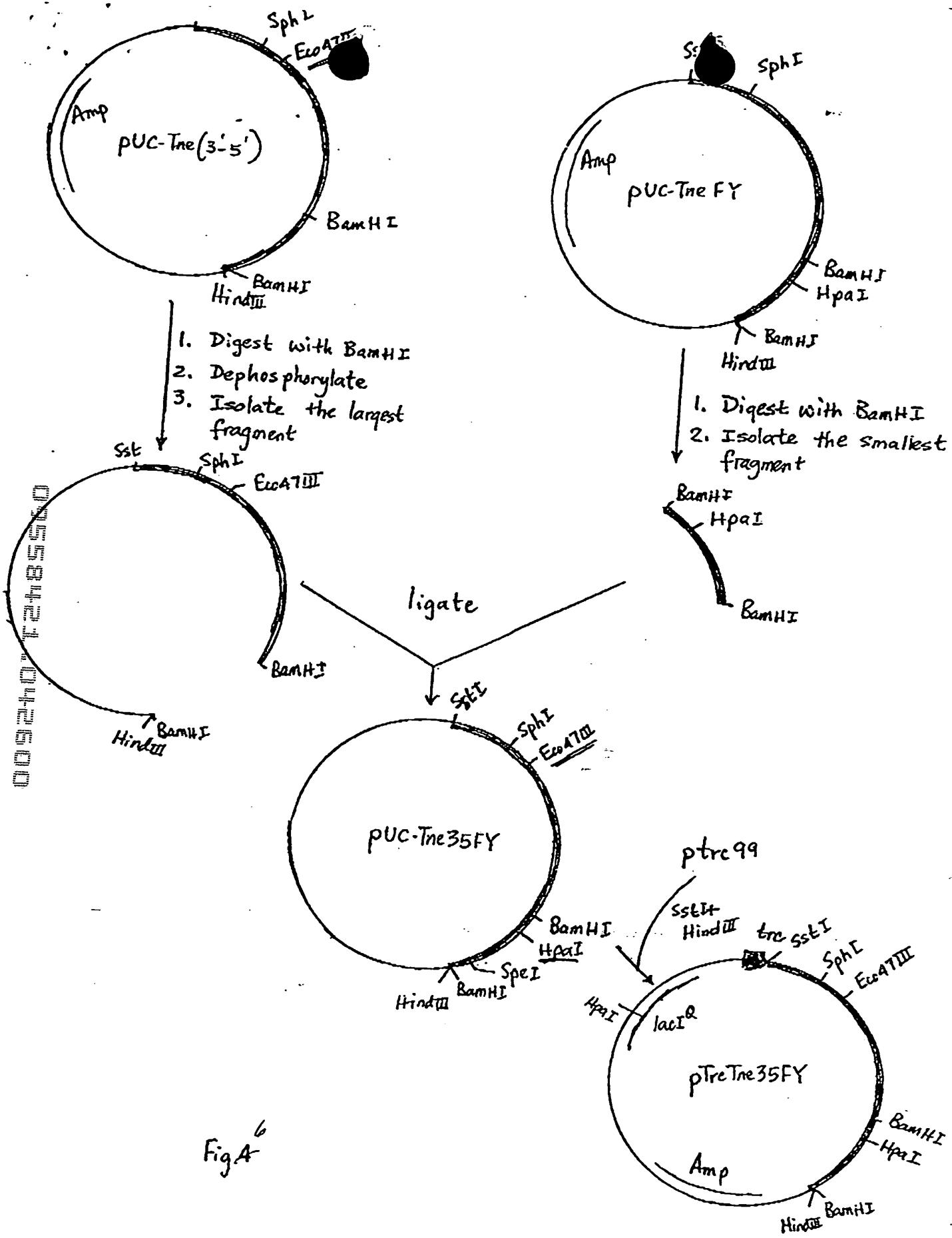


Fig. 3A





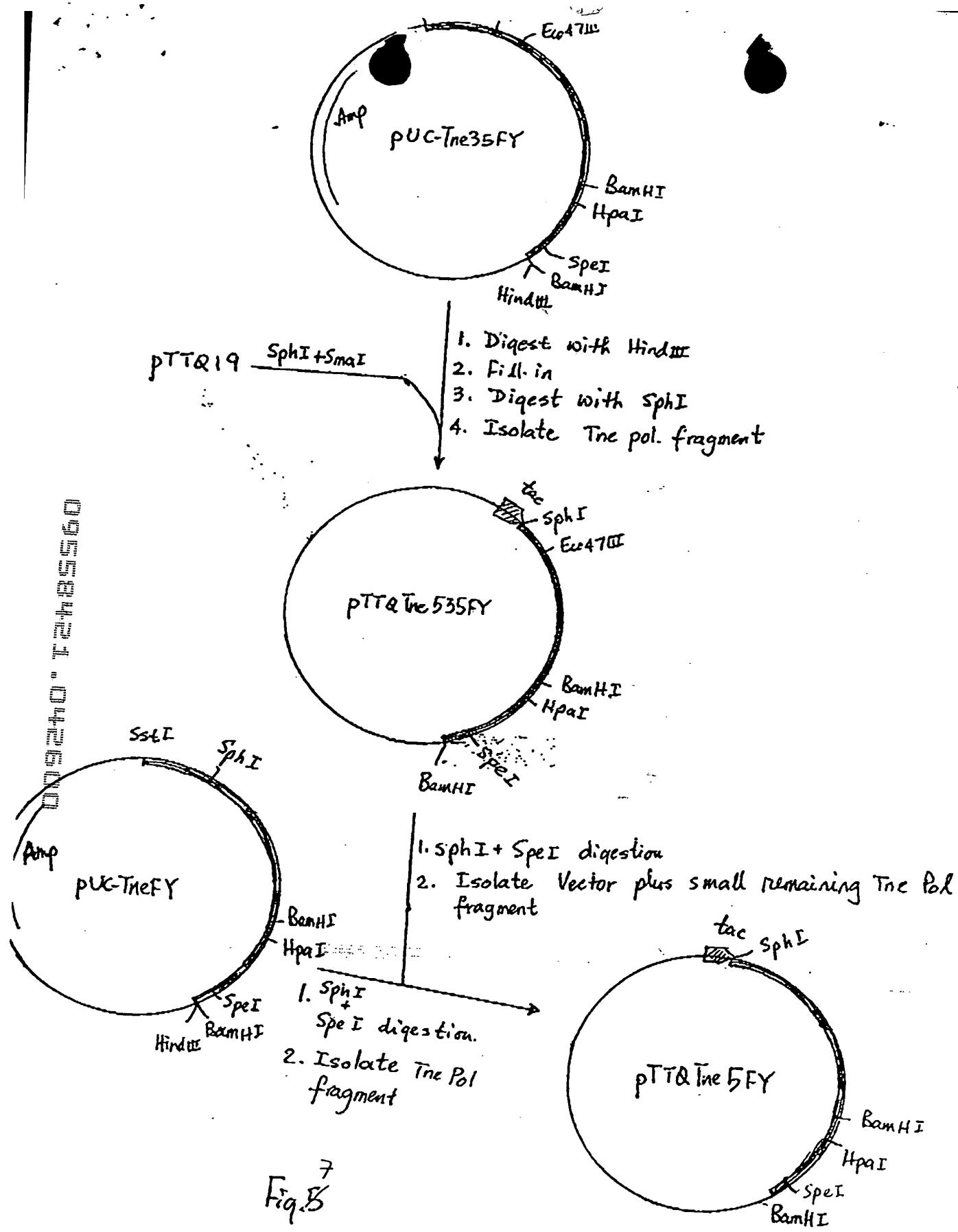


Fig. 8